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<110> Chory, Joanne Jianming, Li Salk Institute for Biological Studies <120> RECEPTOR KINASE, BIN 1 <130> SALKINS.012CP1 <150> 08/881,706 <151> 1997-06-24 <160> 2 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 4104 <212> DNA <213> Arabidopsis <220> <221> CDS <222> (97)...(3684) <400> 1 cttccacttc ctctgtaatg gtggaaccaa aaccctagat tccccctttc atcttctcta 60 cttcccacac ttttctctct cacaaactct tgagaa atg aag act ttt tca agc Met Lys Thr Phe Ser Ser ttc ttt ctc tct gta aca act ctc ttc ttc tcc ttc ttt tct ctt 162 Phe Phe Leu Ser Val Thr Thr Leu Phe Phe Phe Ser Phe Phe Ser Leu 10 15 tea tit caa get tea dea tet eag tet tita tae aga gaa ate eat eag 210 Ser Phe Gln Ala Ser Pro Ser Gln Ser Leu Tyr Arq Glu Ile His Gln 30 ctt ata agc ttc aaa gac gtt ctt cct gac aag aat ctt ctc cca gac 258 Leu Ile Ser Phe Lys Asp Val Leu Pro Asp Lys Asn Leu Leu Pro Asp 45 tgg tct tcc aac aaa aac ccg tgt act ttc gat ggc gtt act tgc aga 306 Trp Ser Ser Asn Lys Asn Pro Cys Thr Phe Asp Gly Val Thr Cys Arg 55 gac gac aaa gtt act tog att gat oto ago too aag oot oto aac gto 354 Asp Asp Lys Val Thr Ser Ile Asp Leu Ser Ser Lys Pro Leu Asn Val 75 80 gga tto agt god gtg too tog tot oto etg tot nto acc gga tta gag

Gly	Phe	Ser	Ala 90	Val	Ser	Ser	Ser	Leu 95	Leu	Ser	Leu	Thr	Gly 100	Leu	Glu	
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_				_	act Thr 140			_				_			•	546
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					cgc Arg 220	_										786
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_				_	atc Ile								-			862
					tgc Cys											930
			_		cca Pro			_		_			_			978
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	-		_	-	gtg Val	-				_			_	_		2850
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		_			gtg Val 940						_		_		_	2946
					aat Asn											2994
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3714

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Phe	Asn	Asp	Leu 500	Thr	Gly	Glu	Ile	Pro 505	Ser	Glγ	Leu	Ser	Asn 510	Cys	Thr
Asn	Leu	Asn 515	Trp	Ile	Ser	Leu	Ser 520	Asn	Asn	Arg	Leu	Thr 525	Glγ	Glu	Ile
Pro	Lys 530	Trp	Ile	Gly	Arg	Leu 535	Glu	Asn	Leu	Ala	Ile 540	Leu	Lys	Leu	Ser
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Asn Leu Ser Gly Pro Ile Pro Glu Met Gly Gln Phe Glu Thr Phe Pro 745 Pro Ala Lys Phe Leu Asn Asn Pro Gly Leu Cys Gly Tyr Pro Leu Pro 760 Arg Cys Asp Pro Ser Asn Ala Asp Gly Tyr Ala His His Gln Arg Ser 775 His Gly Arg Arg Pro Ala Ser Leu Ala Gly Ser Val Ala Met Gly Leu 790 795 Leu Phe Ser Phe Val Cys Ile Phe Gly Leu Ile Leu Val Gly Arg Glu 805 810 Met Arg Lys Arg Arg Lys Lys Glu Ala Glu Leu Glu Met Tyr Ala 825 Glu Gly His Gly Asn Ser Gly Asp Arg Thr Ala Asn Asn Thr Asn Trp 840 Lys Leu Thr Gly Val Lys Glu Ala Leu Ser Ile Asn Leu Ala Ala Phe 855 860 Glu Lys Pro Leu Arg Lys Leu Thr Phe Ala Asp Leu Leu Gln Ala Thr 875 870 Asn Gly Phe His Asn Asp Ser Leu Ile Gly Ser Gly Gly Phe Gly Asp 885 890 Val Tyr Lys Ala Ile Leu Lys Asp Gly Ser Ala Val Ala Ile Lys Lys 905 900 Leu Ile His Val Ser Gly Gln Gly Asp Arg Glu Phe Met Ala Glu Met 915 920 Glu Thr Ile Gly Lys Ile Lys His Arg Asn Leu Val Pro Leu Leu Gly 935 940 Tyr Cys Lys Val Gly Asp Glu Arg Leu Leu Val Asn Glu Val Met Lys 950 955 Tyr Gly Ser Leu Glu Asp Val Leu Gln Asp Pro Lys Lys Gly Gly Val 965 970 Lys Leu Lys Leu Ser Thr Arq Arq Lys Ile Ala Ile Gly Ser Ala Arq 985 Gly Leu Ala Phe Leu His His Asn Cys Ser Pro His Ile His Arg 1000 1005 Asp Met Lys Ser Ser Asn Val Leu Leu Asp Glu Asn Leu Glu Ala Arg 1010 1015 1020 Val Ser Asp Phe Gly Met Ala Arg Leu Met Ser Ala Met Asp Thr His 1030 1035 1040 Leu Ser Val Ser Thr Leu Ala Gly Thr Pro Gly Tyr Val Pro Pro Glu 1050 1055 1045 Tyr Tyr Gln Ser Phe Arg Cys Ser Thr Lys Gly Asp Val Tyr Ser Tyr 1060 1065 Gly Val Val Leu Leu Glu Leu Leu Thr Gly Lys Arg Pro Thr Asp Ser 1080 Pro Asp Phe Gly Asp Asn Asn Leu Val Gly Trp Val Lys Gln His Ala 1095 1100 Lys Leu Arg Ile Ser Asp Val Phe Asp Pro Glu Leu Met Lys Glu Asp 1105 1110 1115 1120 Pro Ala Leu Glu Ile Glu Leu Leu Gln His Leu Lys Val Ala Val Ala 1125 1130 Cys Leu Asp Asp Arg Ala Trp Arg Arg Pro Thr Met Val Gln Val Met 1150 1140 1145 Ala Met Phe Lys Glu Ile Gln Ala Gly Ser Gly Ile Asp Ser Gln Ser 1160 Thr Ile Arg Ser Ile Glu Asp Gly Gly Phe Ser Thr Ile Glu Met Val

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